REMARKS

In response to the Restriction Requirement, applicants have canceled claims 1-22 and 26 without prejudice (see below).

Applicants have amended claim 23 to recite particular IMPDH molecules or molecular complexes. Support for this amendment is found throughout the specification as originally filed, e.g., at page 26, line 29 to page 27, line 9 and page 16, lines 3-15.

Applicants have added claims 27-36. Support for these claims is found throughout the specification as originally filed, e.g., at page 26, line 29 to page 27, line 9 and page 16, line 16 to page 19, line 12.

Applicants have submitted herewith Exhibit A, marked up claims showing the amendments. In Exhibit A, the added portions are underlined and the deleted portions are bracketed.

Claims 23-25 and 27-36 are now pending.

None of these amendments add new matter.

The Drawings

The Drawings have been objected to by the Draftsperson for the reasons given in the Notice of Draftsperson's Patent Drawing Review (copy enclosed). Pursuant to 37 C.F.R. § 1.185, applicants have submitted herewith formal drawings amended according to the Draftsperson's instructions.

The Restriction Requirement

The Examiner has required restriction of the claims under 35 U.S.C. § 121 into one of the following groups:

Group I:	An IMPDH molecule or molecular complex (claims 1-11);
Group II:	A machine-readable data storage medium for displaying a 3-dimensional model of IMPDH (claims 12-21);
Group III:	A machine-readable data storage medium directed to a Fourier transformation of at least a portion of IMPDH as compared to an unknown molecule or complex (claim 22);
Group IV:	A method for evaluating the ability of a chemical entity to associate with an IMPDH molecule or molecular complex (claim 23);
Group V:	A method of utilizing molecular replacement via IMPDH structure to generate at least a portion of an unknown structure (claims 24-25);
Group VI:	A method of preparing an IMPDH/XMP*/MPA crystal (claim 26).

The Examiner contends that the Group I, Group II, Group III, Group IV, Group V, and Group VI inventions are distinct. Specifically, the Examiner contends that Group I and Groups II-V are "related as product and process of use or products of use," and that the inventions of Groups II-V are "directed to differing modeling practice specialties." The Examiner further contends that the inventions of Groups I and VI are "related as product made and process of making." Applicants have canceled claims within Groups I, II, III, and VI (i.e. claims 1-22 and 26). Applicants traverse this restriction with respect to Groups IV and V and submit that claims 23-25 therein should be examined together for the reasons set forth below.

Applicants traverse the restriction with respect to Groups IV and V on the basis of the procedures set forth in the Manual for Patent Examining Procedure ("MPEP").

The MPEP states that there are two criteria for a proper requirement of restriction. MPEP § 803. The first is that the inventions must be independent or distinct as claimed. The second is that there must be a serious burden on the Examiner if restriction is not required. The MPEP further states that "[i]f the search and examination of an entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to independent or distinct inventions." MPEP § 803.

The Examiner states that the methods of Groups IV and V are directed to distinct usage or products because "Group IV is directed to ligand binding modeling to whatever 3-dimensional structure is desired" and "Group V is directed to the practice of replacement to define an unknown structure." Whether the Examiner is correct in his "distinctness" contention is irrelevant in this instance. Here, there is no serious burden for the Examiner to search the claims of both Groups IV and V because these searches overlap extensively, such that a search for the method of evaluating the ability of a chemical entity to associate with an IMPDH molecule or molecular complex of Group IV would reveal any art relating to the method of utilizing molecular replacement via IMPDH structure of Group V. Furthermore, Groups IV and V are both classified in class 702, subclass 19. For these reasons, applicants request that Group IV and V be rejoined.

Applicants request that the Examiner examine rejoin Groups IV and V. If the Examiner does not agree with applicants' proposal to rejoin Groups IV and V, applicants provisionally elect with traverse the claims of Group IV for initial substantive examination. 37 C.F.R. § 1.143. This election is made expressly without waiver of applicants' rights to file for and obtain claims directed to the non-elected subject matter in divisional or

continuing applications claiming priority and benefit from this application under 35 U.S.C. § 120.

In view of the above, applicants request that the Examiner examine claims 23-25 and 27-36 in this application. Applicants request favorable consideration and early allowance of the pending claims.

Respectfully submitted,

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EXHIBIT A

MARKED UP CLAIMS SHOWING THE AMENDMENTS

23. (Amended) A method for evaluating the ability of a chemical entity to associate with a molecule or molecular complex [according to any one of claims 1 to 11] comprising all or any part of a binding pocket defined by structure coordinates of IMPDH amino acids 68, 69, 93, 273, 274, 275, 276, 277, 303, 322, 324, 325, 326, 327, 328, 330, 331, 332, 333, 334, 337, 339, 340, 364, 413, 414, 415, 416, 420, 439, 440, 441, 442, 469, and 470 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, comprising the steps of:

a. employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; and

b. analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket.

27. (Added) The method according to claim 23, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 274, 275, 276, 277, 303, 322, 324, 325, 326, 331, 333, 414, 415, and 441 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation

from the backbone atoms of said amino acids of not more than 1.5 Å.

28. (Added) The method according to claim 27, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 275, 276, 303, 325, 326, 331, 333 and 441 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

29. (Added) A method for evaluating the ability of a chemical entity to associate with a molecule or molecular complex comprising all or any parts of a binding pocket defined by structure coordinates of IMPDH amino acids 67, 68, 69, 70, 73, 274, 275, 276, 303, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 364, 365, 366, 367, 368, 385, 386, 387, 388, 389, 391, 411, 412, 413, 414, 415, 416, 419, 440, 441, 442, 443, 500, 501, 502, 503, 504, 505, and 506 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, comprising the steps of:

a. employing computational means to perform a fitting operation between the chemical entity and a binding pocket of the molecule or molecular complex; and

b. analyzing the results of said fitting operation to quantify the association between the chemical entity and the binding pocket.

30. (Added) The method according to claim 29, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 68, 69, 70, 303, 322, 326, 327, 328, 329, 330, 331, 332, 333, 335, 364, 365, 366, 367, 385, 386, 387, 388, 411, 413, 414, 415, 416, 419, 441, 442, 443, 501, 502, 503, and 504 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

31. (Added) The method according to claim 30, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 68, 70, 322, 328, 329, 331, 332, 335, 364, 366, 387, 388, 411, 413, 414, 415, 441, 442, 501, and 502 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

32. (Added) The method according to claim 29, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 67, 68, 69, 70, 73, 93, 273, 274, 275, 276, 277, 303, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 337, 339, 340, 364, 365, 366, 367, 368, 385, 386, 387, 388, 389, 391, 411, 412, 413, 414, 415, 416, 419, 420, 439, 440,

441, 442, 443, 469, 470, 500, 501, 502, 503, 504, 505, and 506 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

33. (Added) The method according to claim 32, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 68, 69, 70, 274, 275, 276, 277, 303, 322, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 335, 364, 365, 366, 367, 385, 386, 387, 388, 411, 413, 414, 415, 416, 441, 442, 443, 501, 502, 503, and 504 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

34. (Added) The method according to claim 33, wherein said binding pocket is defined by structure coordinates of IMPDH amino acids 68, 70, 275, 276, 303, 322, 325, 326, 328, 329, 331, 332, 333, 335, 364, 366, 387, 388, 411, 413, 414, 415, 441, 442, 501, and 502 according to Figure 1, or a homologue of said molecule or molecular complex, wherein said homologue comprises a binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

35. (Added) The method according to claim 32, wherein said molecule or molecular complex is defined by the set of structure coordinates according to Figure 1,

or a homologue thereof, wherein said homologue has a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

36. (Added) The method according to claim 32, wherein said molecule or molecular complex comprises amino acids 1-514 of IMPDH, XMP*, and MPA.